

EXPRESS MAIL
EL360933793US
ATTY. DKT. 266/187
SHEET 1 OF 11

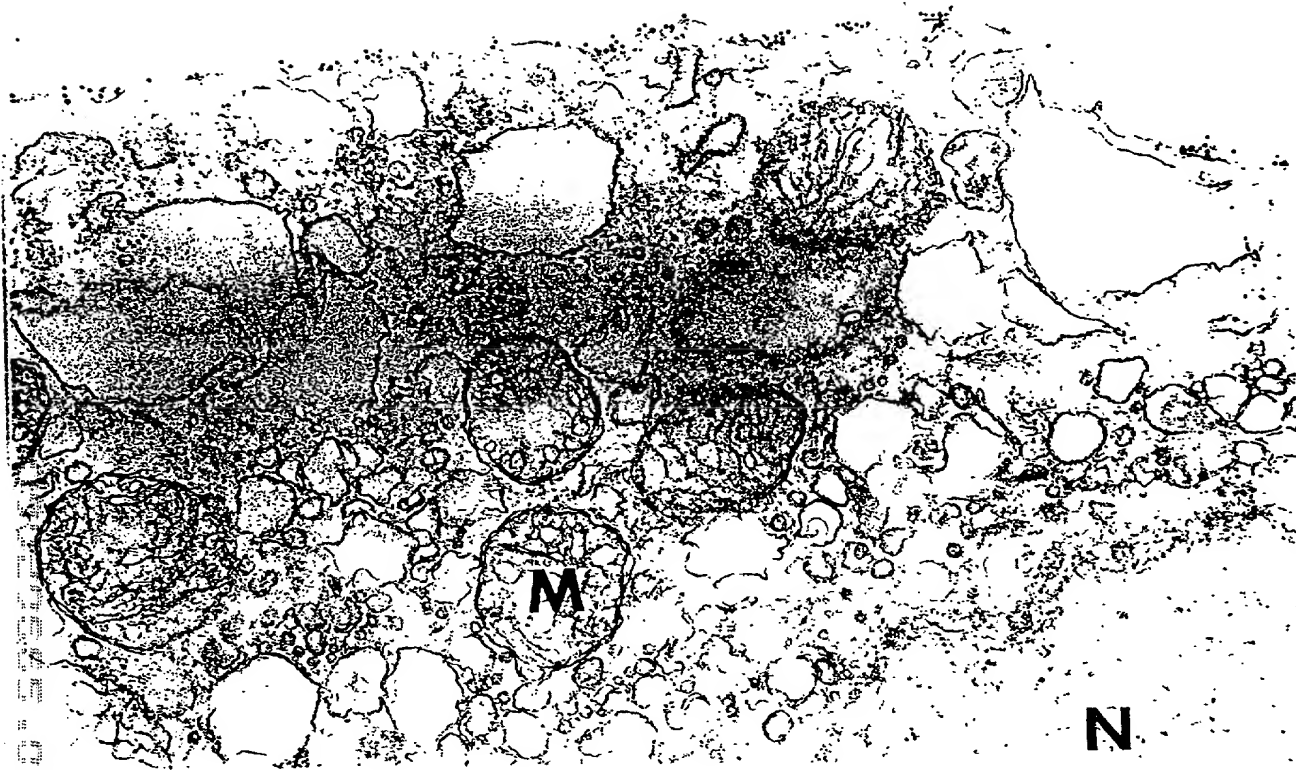


FIGURE 1

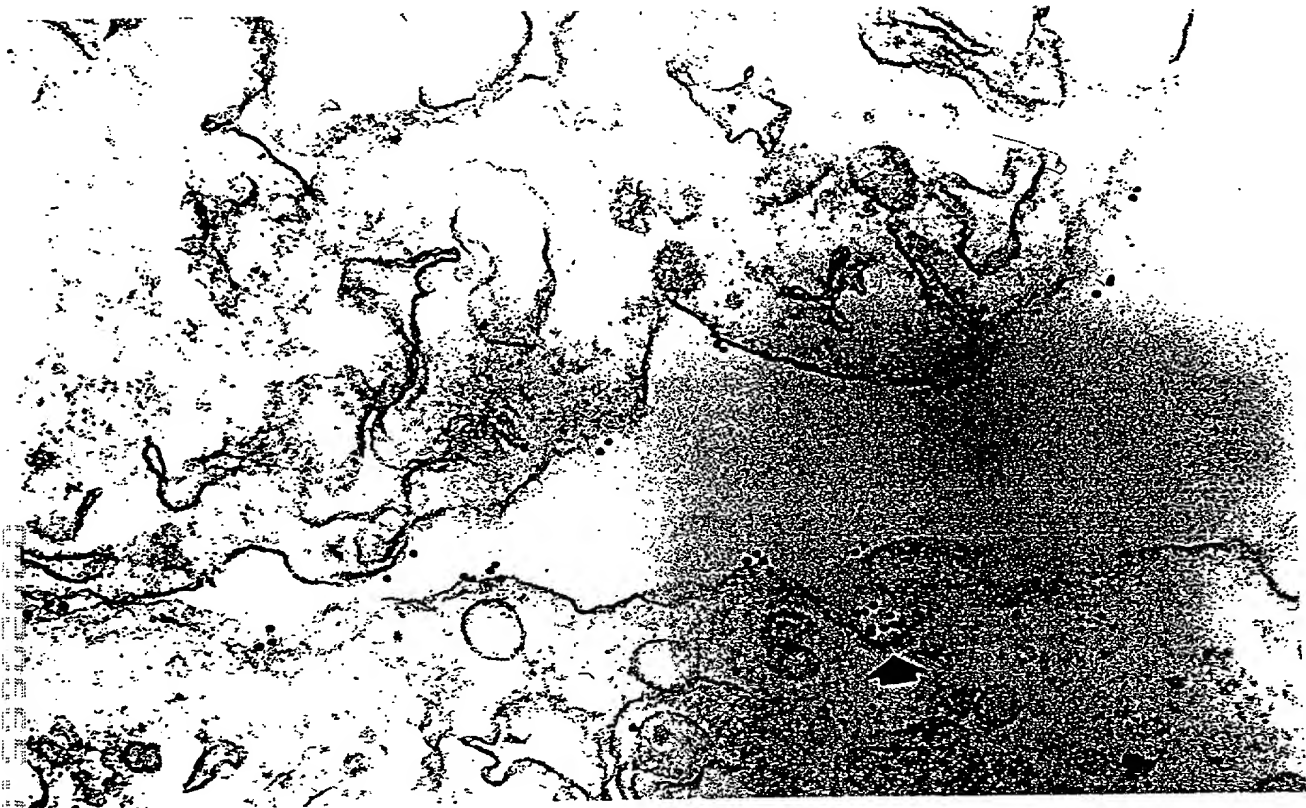


FIGURE 2

EXPRESS MAIL
EL360933793US
ATTY. DKT. 266/187
SHEET 3 OF 11



FIGURE 3

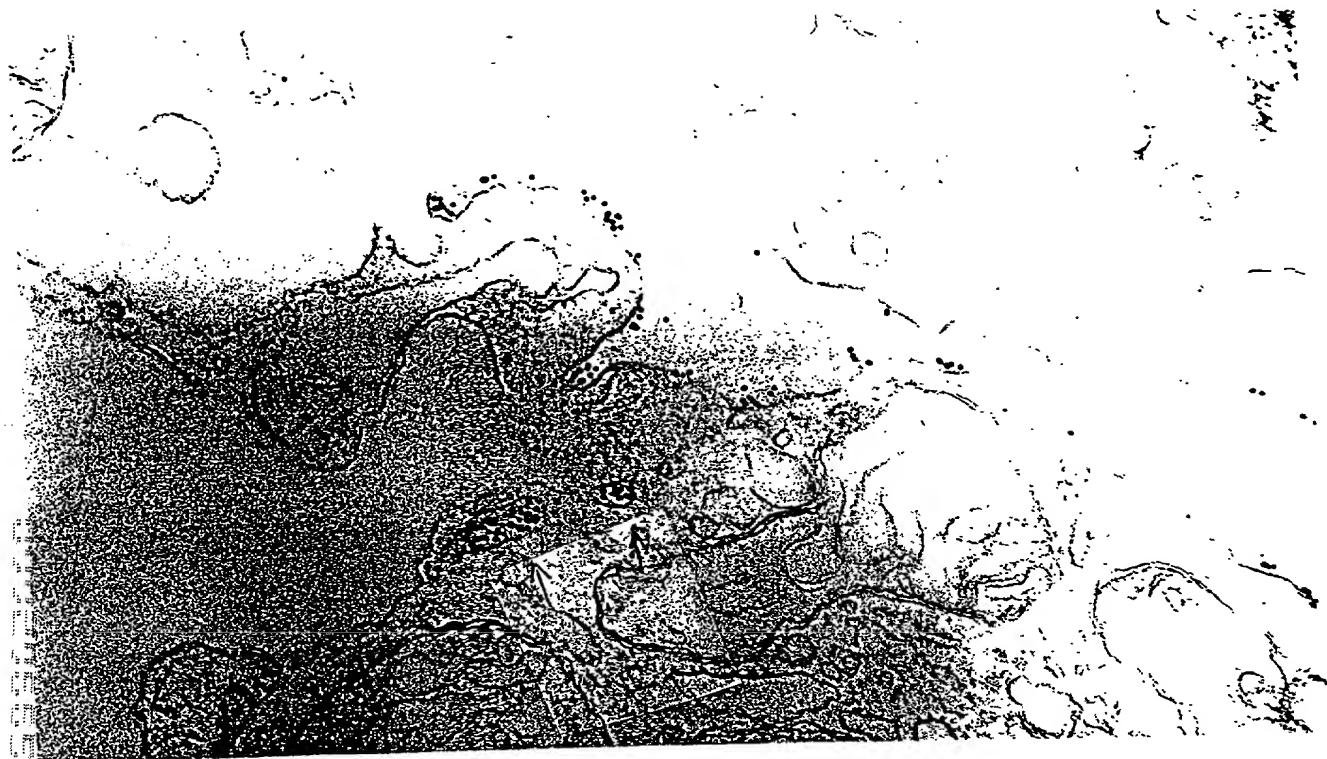


FIGURE 4



FIGURE 5

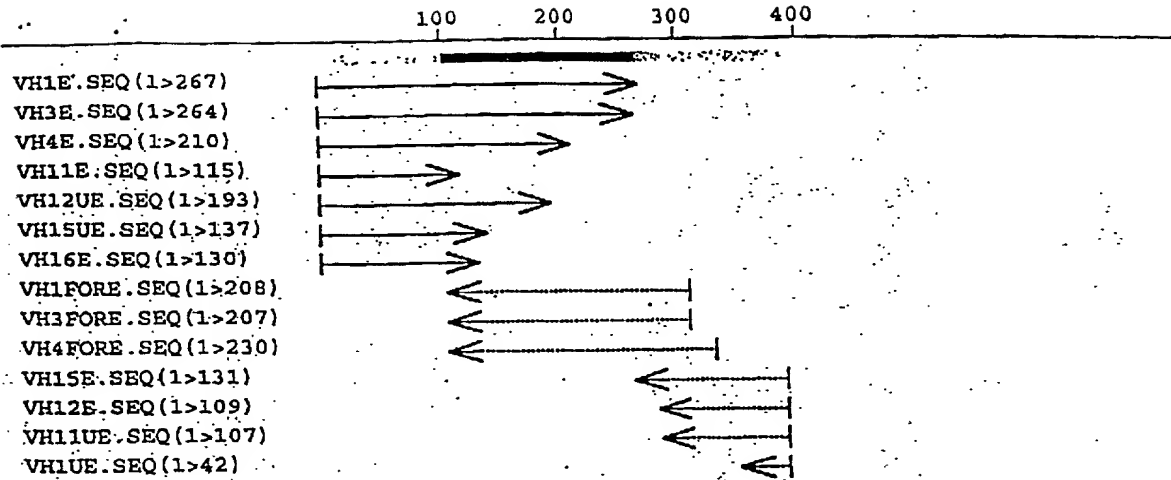


FIGURE 6

Enzymes: All 74 enzymes (No Filter)
Settings: Linear, Certain Sites Only, Standard Genetic Code

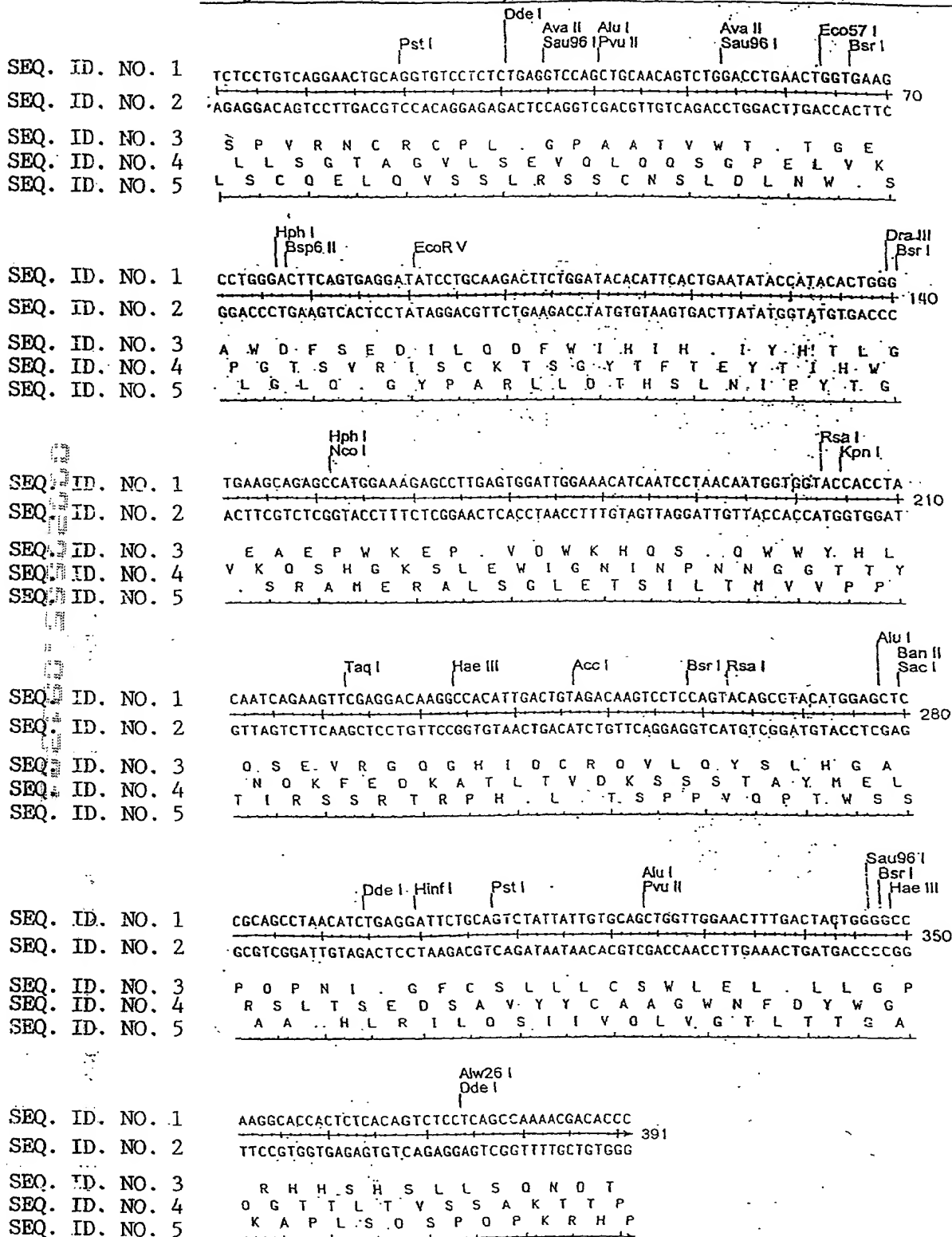


FIGURE 7

Lipman-Pearson Protein Alignment

Ktuple: 2; Gap Penalty: 4; Gap Length Penalty: 12

Seq1(1>115)	Seq2(1>125)	Similarity Index	Gap Number	Gap Length	Consensus Length
J591VH.PRO	MUVHIIA.PRO				
(1>115)	(1>125)	75.6	2	10	125

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      10      20      30      40      50
EVQLQQSGPELVKPGTSVRISCKTSGYTFTEYTI-HWVKQSHGKSLEWIGNINPNNGGTT
EVQLQQSGPELVKPG:SV:ISCK:SGYTFT:Y : :WVKQS.GKSLEWIG:INP.NGGT:
EVQLQQSGPELVKPGASVKISCKASGYTFTDYYMNNWVKOSPGKSLEWIGDINPGNGGTS
      10      20      30      40      50      60
60      70      80      90      100      110
YNQKFEDKATLTVDKSSSTAYMELRSLTSEDSAVYYCAAG-----WNFDYWGQGTT
YNQKF:KATLTVDKSSSTAYM:L.SLTSEDSAVYYCA G ..FDYWGQGTT
YNQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARGYYSSSYMAYYAFDYWGQGTT
      70      80      90      100      110      120

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LTVSS
 :TVSS
 VTVSS

FIGURE 8

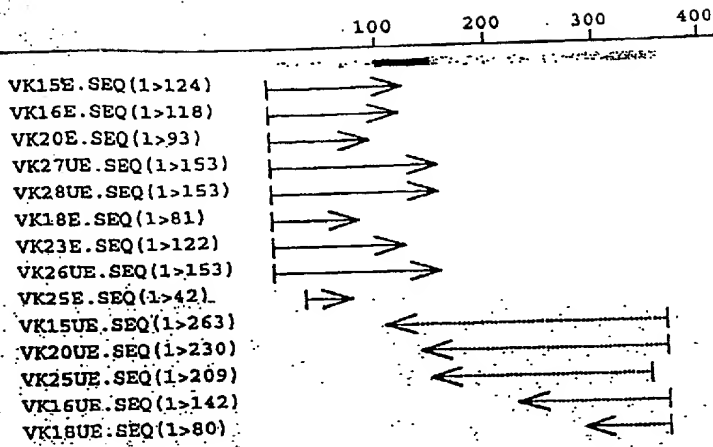


FIGURE 9

Enzymes: All 74 enzymes (No Filter)
Settings: Linear, Certain Sites Only, Standard Genetic Code

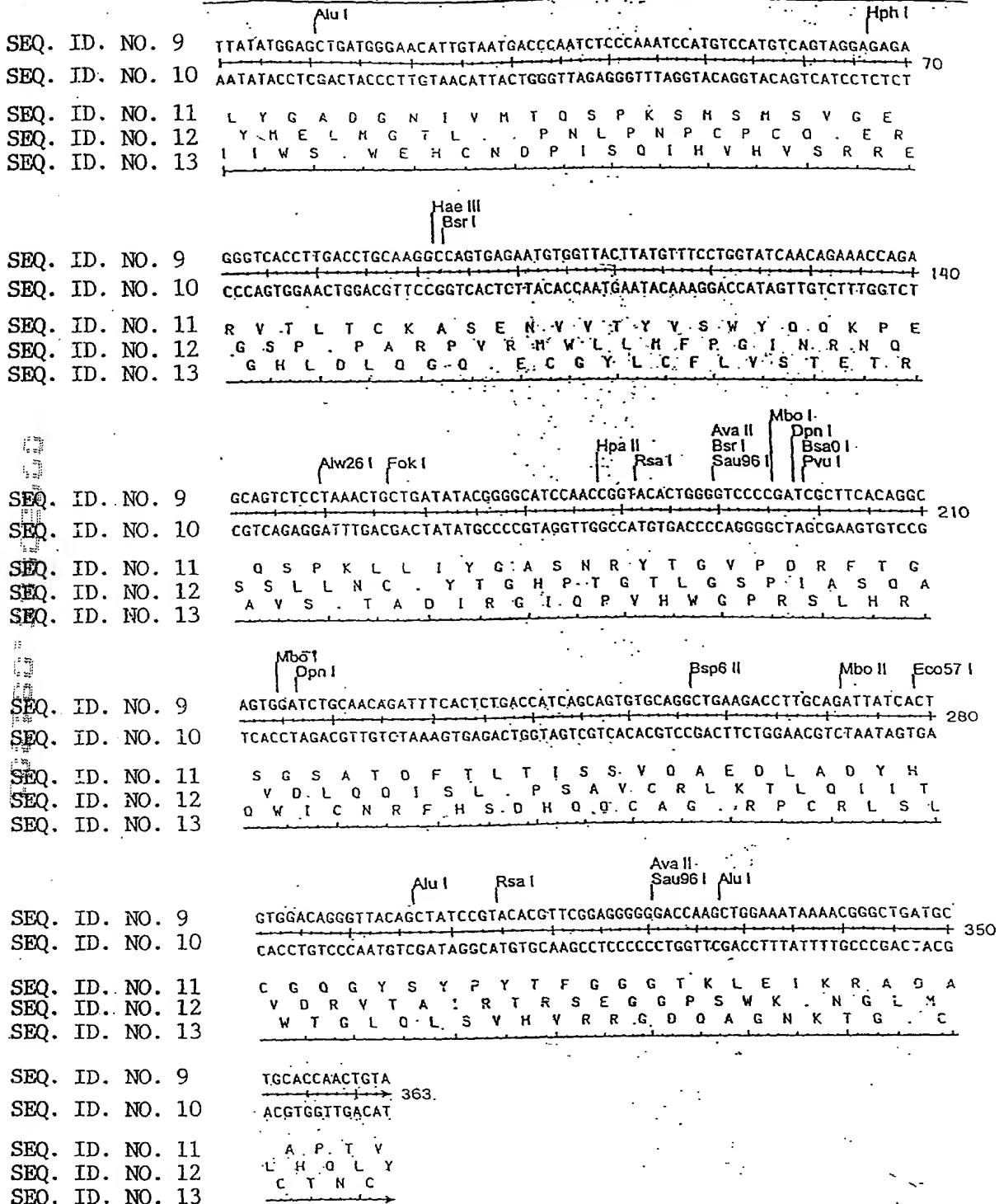


FIGURE 10

Lipman-Pearson Protein Alignment

Ktuple: 2; Gap Penalty: 4; Gap Length Penalty: 12

Seq1(1>107)	Seq2(1>111)	Similarity Index	Gap Number	Gap Length	Consensus Length
J591VK.PRO	MUVKV.PRO				
(1>107)	(1>109)	60.4	2	2	109
10 20 30 40 50 NIVMTQSPKSMMSVGERVTLTCKAS-ENVVTYVSWYQOKPEQSPKLLIYGASNRYTGVP :I MTQSP.S:S S:G:RVT:TC:AS ::: Y::WYQOKP. SPKLLIY AS. :GVP DIOMTQSPSSLSASLGDRVTITCRASQDDISNYLNWYQOKPGGSPKLLIYYASRLHSGVP 10 20 30 40 50 60 60 70 80 90 100 DRFTGSGSATDFTLTISVVOAEDLADYHCGGYSY-PYTFGGGKLEIK .RE:GSGS:TD::LTIS:::ED:A.Y C QG:: P TFGGKLEIK SRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPRTFGGKLEIK 70 80 90 100					

FIGURE 11